

Novel Point Mutation in the Uroporphyrinogen III Synthase Gene Causes Congenital Erythropoietic Porphyrria of a Japanese Family

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The molecular basis of the uroporphyrinogen III synthase (UROHIS) deficiency was investigated in a member of a Japanese family. This defect in heme biosynthesis is responsible for a rare autosomal recessive disease: congenital erythropoietic porphyria (CEP) or Günther's disease. The patient was homozygous for a novel missense mutation: a G to T transition of nucleotide 7 that predicted a valine to phenylalanine substitution at residue 3 (V3F). The parents were heterozygous for the same mutation. The loss of UROHIS activity was verified by an in vitro assay system. The corresponding mutated protein was expressed in *Escherichia coli* and no residual activity was observed. Further studies are needed to determine whether the mutations of the UROHIS gene (*UROS*) have a specific profile in Japan compared to European or American countries. *Am. J. Med. Genet.* 70:299–302, 1997.

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INTRODUCTION

Porphyrias are a group of inherited disorders caused by specific defects along the heme biosynthetic pathway [Kappas et al., 1989]. Congenital erythropoietic porphyria (CEP), or Günther's disease, is a rare disorder inherited as an autosomal recessive mode. The in-

cidence of this disease is not known, but is exceedingly low; less than 200 cases were reported [Moore et al., 1987; Kappas et al., 1989]. CEP is characterized by severe cutaneous photosensitivity, chronic hemolysis, and massive porphyrinuria, resulting from the accumulation in the bone marrow, peripheral blood, and other organs of large amounts of predominantly type I porphyrins, which are not substrates for heme synthesis [Romeo and Levin, 1969; Deybach et al., 1980; Moore et al., 1987; Kappas et al., 1995]. A characteristic abnormality of the disease is an 80–98% reduction in the activity of uroporphyrinogen III synthase (UROHIS), the fourth enzyme of the heme biosynthetic pathway (EC. 4.2.1.75) [Romeo and Levin, 1969; Deybach et al., 1981].

Since the cDNA of the UROHIS has been cloned and sequenced by Tsai and co-workers [1988], attention has focused on the molecular defects responsible for CEP. To date, 17 different mutations of the UROHIS gene (*UROS*) have been described [Deybach et al., 1990; Boulechar et al., 1992; Warner et al., 1992; Bensidhoum et al., 1995; Xu et al., 1995; Tanigawa et al., 1996] and a single mutation, C73R, is present in 50% of the disease alleles in the Europeans and is associated with a severe phenotype. In Japan, we have recently reviewed 33 cases of CEP and found that only 4 cases are analyzed at the molecular level [Xu et al., 1995; Tanigawa et al., 1996]. Identification of mutations of *UROS* is important for genetic counseling and prenatal diagnosis of affected families [Ged et al., 1996].

In this study, we describe the identification of a novel *UROS* mutation in a Japanese family and we show that the base change is disease-causing mutation, through heterologous expression in *E. coli*.

MATERIALS AND METHODS

Case Report

We studied a CEP man, who lived in the Fukushima prefecture of Japan and his family members, after obtaining informed consents. The family pedigree is shown in Figure 1. The patient, a 34-year-old male, had

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classical manifestations of CEP, starting shortly after birth. High performance liquid chromatography of urine also showed a porphyrin excretion profile predominantly of Type I isomers in the patient. UROHIS enzyme activity was not measurable (<2% of the normal value) in the erythrocytes of the patient. Both parents have 50% residual activity (Fig. 1).

UROHIS Assay in Erythrocytes

UROHIS activity was determined by the enzyme coupled assay described previously with modifications [Deybach et al., 1981]. Whole blood (10 μ l) were sonicated on ice in 250 μ l of 100 mM Tris-Cl, pH 8.0, containing 1 mM EDTA and 1% Tween. Aliquots of the 12,000g supernatant were incubated with porphobilinogen and the amount of porphobilinogen deaminase (or hydroxymethylbilane synthase) catalyzing the formation of 200 pmoles of uroporphyrinogen in the assay conditions. Partially purified porphobilinogen deaminase was prepared by heating a human hemolysate at 60°C for 90 minutes. The incubation mixture for the UROHIS assay contains 25 nmol porphobilinogen, 250 nmol dithiothreitol, 75 μ l porphobilinogen deaminase (corresponding to the formation of 200 pmoles of uroporphyrinogen), 5 to 50 μ l of hemolysates, and 2.5 μ mol of Tris-Cl, pH 8.0, in a total volume of 250 μ l. Incubation was carried out at 37°C for 15 minutes in the dark. The reaction was stopped by addition of 25 μ l of 50% trichloroacetic acid. The oxidized uroporphyrin isomers were separated by C18 reversed phase high performance liquid chromatography using 15% acetonitrile in 1 M ammonium acetate buffer, pH 5.2, and quantitated using a spectrofluorimeter as a detector. Porphyrins were detected by their fluorescent emission at 618 nm after excitation at 404 nm. One unit of UROHIS activity was defined as the amount of enzyme which formed 1 nanomole of uroporphyrinogen III per hour at 37°C. Enzyme assay in the bacterial lysate was measured as previously described [Boulechar et al., 1992; Bensidhoum et al., 1995].

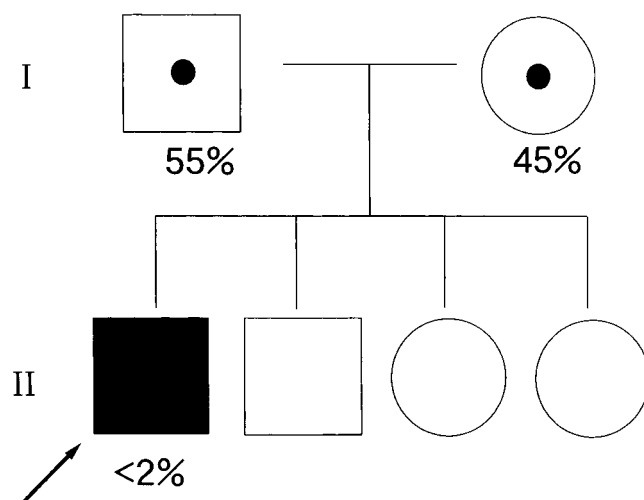


Fig. 1. Pedigree of the Japanese family. Percentage is UROHIS erythrocyte activity for the patient and parents. Enzyme activity in normal erythrocytes is 5.36 \pm 1.34 (SD) U/mg protein.

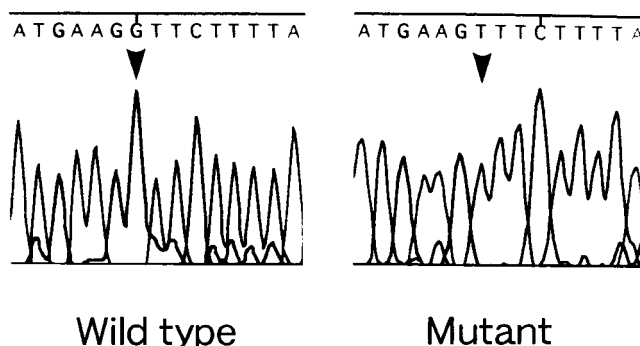


Fig. 2. Fluorescence based dye-primer sequencing was performed on the last exonic fragment of the gene, amplified by PCR genomic DNA. Patient is homozygous for a G to T change at codon 7 (V3F, left panel) as well as her mother, while her father has a normal allele (right panel).

Genomic DNA Extraction and Polymerase Chain Reaction (PCR)

Genomic DNA was extracted from peripheral blood leukocytes using DNA Extractor WB Kit (Wako Pure Chemical Industries, Japan) and each exon including its intron-exon boundaries was amplified by PCR using primer sets previously described [Warner et al., 1992; Bensidhoum et al., 1995; Xu et al., 1995]. Amplified PCR products were purified on 1% agarose gels by QIAx kit (QIAGEN, Germany).

Subcloning and DNA Sequencing

For the sequencing, purified PCR products were ligated to the pCRTMII vector (TA cloning kit, Invitrogen Corporation, La Jolla, CA) and chimeric vectors were used to transform competent *E. coli* cells. Fifteen colonies of each exon were picked up and after small scale preparation of plasmid DNA, the products were purified by FlexiPrep Kit (Pharmacia Biotech, Sweden), subjected to a fluorescence-based dye primer sequence reaction with a PRISMTM Ready Reaction dye Primer Cycle Sequencing Kit (Perkin-Elmer, Oak Brook, IL), and then sequenced with a Thermo Sequenase Core Sequencing Kit (Amersham International, England) and a Hitachi SQ-5500DNA Sequencer (Hitachi Electronics Engineering Co., Japan).

Construction and Functional Expression of the Mutant UROHIS cDNA

The mutant UROS-cDNA was constructed with Ex-Site PCR-Based Site-Directed Mutagenesis kit (Stratagene, La Jolla, CA) according to the manufacture's instruction. The wt-UROS-cDNA [Boulechar et al., 1992] in the bacterial expression vector pKK223-3 (Pharmacia Biotech, Sweden) was used as a template. The oligonucleotide primers used were 5'-ATAATGAAGTTTCTTTTACTG-3' (sense, nucleotide -3 to +18) and 5'-TGCCTGGCAGGCCCTTATAGGG-3' (antisense, -4 to -24), where the mutated nucleotide is underlined, and the italics is a *Stu*I restriction site that allows selecting the clones harbouring the mutation. The mutated and adjacent regions were confirmed by sequencing. The resultant plasmid was designated pKK-UROHIS-V3F. *E. coli* cells were transformed with

TABLE I. Specific Activity of Normal and Mutated UROHIS Proteins*

Plasmid	Specific activity (U/mg protein)		Number of assays	Residual activity
	Mean	SD		
pKK	0.35	±0.1	5	—
pKK-UROHIS (wt)	143	±35	4	100
pKK-UROHIS (V3F)	0.37	±0.9	3	<2

*Results of specific activity (SA) are the mean of three to five experiments. Residual activity was determined by dividing $100 \times [SA - SA(pKK)]$ by $[SA(pKK - UROHIS) - SA(pKK)]$.

pKK-UROHIS-V3F or pKK-wt-UROHIS and grown at 37°C. The protein expression was then induced by growing the cells in the presence of IPTG as previously described [Boulechar et al., 1992; Bensidhoum et al., 1995]. UROHIS specific activity (SA) is expressed as the relative amount of UROHIS (nmoles) formed in 1 hour/mg of protein. Results are the mean of three to five experiments. Residual activity (as a percentage of the normal UROHIS specific activity) was determined by dividing $100 \times [SA - SA(pKK)]$ by $[SA(pKK-UROHIS) - SA(pKK)]$ where SA(pKK) and SA(pKK-UROHIS) are the specific activities of the lysate (empty plasmid) and of the normal UROHIS protein respectively.

RESULTS

The coding region of *UROS* had a normal size in the patient. In the patient, a single mutation was found at a homozygous state: a G to T change at nucleotide 7 leading to a valine to phenylalanine substitution at codon 3 (V3F), as shown in Figure 2. Furthermore, in both parents of this patient, the same mutation was found at the heterozygous state. This is not surprising since they were suspected to be a strong consanguinity based on the same geographic area in Japan, the Fukushima Prefecture.

In order to demonstrate that this base change is a disease-causing mutation, the corresponding mutated protein was expressed in *E. coli*. The activity of UROHIS was measured in the bacterial lysate as previously described [Boulechar et al., 1992; Bensidhoum et al., 1995]. No residual activity was observed in the mutated construct as compared to the normal pKK-UROHIS (<2% of normal activity) (Table I).

DISCUSSION

To date, 17 different mutations in UROHIS have been described in CEP patients: L4F, Y19C, T53M, T62A, A66V, C73R, V82F, V99A, A104V, 633insA, G225S, T228M, Q249X, IVS2⁺, IVS9^{ΔA+4}, 148del98, and 60ins80A [Deybach et al., 1990; Boulechar et al., 1992; Warner et al., 1992; Bensidhoum et al., 1995; Xu et al., 1995; Tanigawa et al., 1996]. A single mutation, C73R, has been frequently reported in European and American countries [Deybach et al., 1990; Boulechar et al., 1992; Warner et al., 1992; Verstraeten et al., 1993; Bensidhoum et al., 1995; Xu et al., 1995; Ged et al., 1996; Tanigawa et al., 1996]. In Asian countries, such as Japan, the mutation C73R has not yet been observed. Recently, three mutations (T62A, T228M,

and Q249X) were reported in Japanese patients [Xu et al., 1995; Tanigawa et al., 1996]. T62A has been observed only once in all CEP patients, and a patient who showed the mutation Q249X [Tanigawa et al., 1996], also present in our pedigree, may not live in the Kyushu Island in Japan.

V3F lesion did not occur at a CpG dinucleotide, a mutation hot spot due to deamination of methylcytosine to thymidine. Furthermore, the mutation V3F substituted isofunctional residues, but it had no residual activity in the bacterial expression system. The corresponding amino acid may play an important role in the function of the enzyme.

The epidemiological and clinical data of all porphyrias in Japan have been summarized [Tanigawa et al., 1995]. It is noticeable that 33 of 200 CEP cases have been reported in Japan. Further studies in Japanese CEP patients are currently performed to determine whether *UROS* mutations have a specific profile in Japan compared to European or American countries. Finally, same as other genetic disorders, a screening of CEP families with mutations at the DNA level will benefit to genetic counseling and prenatal diagnosis. HLA-identical allogeneic bone-marrow transplantation can be proposed to severely affected patients [Kauffman et al., 1991]. Recent studies indicate the potential usefulness of somatic gene therapy in the future for this disease [Moreau-Gaudry et al., 1995].

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